Table S2. List of 62 top gene 'hits' from primary screen

Gene ID	Z-score	# of total shRNA	# of hits with 2-fold increase	Gene ID	Z-score	# of total shRNA	# of hits with 2-fold increase
ACSL4	2.00	8	5	C19orf66	<2	3	2
ATCAY	2.73	3	2	CDKN1A	<2	4	2
ATF3	2.53	2	2	CXCR4	<2	10	4
ATL1	2.58	3	2	DTX3L	<2	4	3
C2orf64	3.01	3	3	EIF2AK2	<2	9	6
CXCL11	124.03	2	2	GBP2	<2	3	2
DDX24	2.07	5	4	GPR126	<2	9	2
EXOC4	2.54	2	2	HRASLS2	<2	3	2
GBP3	2.89	3	2	HTR1D	<2	6	2
GNB4	2.50	4	3	IFI6	<2	2	1
ICAM1	2.81	4	3	IFIT2	<2	4	2
IFI44L	2.07	4	3	IFIT3	<2	2	1
IFITM2	10.75	2	2	IFRD1	<2	4	3
IL4I1	2.13	6	3	IL13RA1	<2	3	2
IRF8	2.35	2	1	IRF1	<2	6	2
IRF9	2.48	3	3	JAK2	<2	4	3
KBTBD8	4.52	7	4	MOV10	<2	11	3
KLK8	3.59	2	2	PAK3	<2	7	2
LPGAT1	2.63	6	5	PSMB9	<2	3	2
MAFK	3.46	4	4	PSME2	<2	4	3
NUB1	3.21	3	2	RGS22	<2	5	2
OAS1	3.02	2	1	SAMD9	<2	3	2
RNASE6	79.82	2	2	SAMD9L	<2	2	1
SAMHD1	2.03	3	1	SC4MOL	<2	3	2
SERPINB7	2.26	5	4	SEMA6D	<2	3	2
STAT2	19.37	3	3	SLC15A3	<2	6	3
TNFSF10	6.20	2	2	SP110	<2	5	2
TNFSF13B	3.30	4	2	TLR3	<2	3	2
TRIM21	2.15	8	6	TRIM25	<2	4	3
AKAP8	<2	10	4	TRIM6	<2	10	4
AKT3	<2	6	2	VISA	<2	3	3

Two criteria were used for selection: (1) 29 genes were selected with Z-scores calculated as equal or greater than 2; and (2) the remaining 33 genes had Z-scores below 2 but there were multiple shRNAs (or one if only two shRNAs available in the library) that resulted in an increased (two-fold over control scrambled shRNA) percentage of cells infected with WNV, as judged by flow cytometry.